IN THE SPECIFICATION:

Insert the following paragraphs at page 7, line 15, of the specification:

Embodiments of the invention include methods for discovering suitable chromatography parameters for the separation of biological molecules, consisting of the following method steps:

a) different chromatography media are arranged in a location dependent manner on a multiwell plate defined by columns (X direction) and rows (Y direction) as matrix, on the matrix points of the plate defined by the matrix in the respective cavities therein, where the chromatography media consists on the one hand of materials (B) which bind the biological sample and on the other hand of materials (NB) which do not bind the biological sample,

b) the different chromatography media are brought into contact with a biological sample in the respective cavities,

c) where the chromatography media are arranged in the individual cavities of the multiwell plate in such a way that on the one hand a chromatography medium from group B and group NB is present in each individual cavity, but on the other hand this chromatography medium from group B and group NB differ at least in a single parameter,

d) the biological sample located in the respective cavities is separated into biomolecules bound to binding materials and biomolecules not bound to binding materials, and

e) the bound and not-bound molecules of the biological sample are

analysed for each individual cavity depending on the chromatography medium located in the respective cavity.

In a preferred embodiment, the biological sample is purified or unpurified proteins, peptides, nucleic acids of all types, carbohydrates, lipids and other biomolecule substance classes or low-molecular-weight metabolism products or mixtures thereof.

In another preferred embodiment, the chromatography media of the materials binding the biological sample (group B) are selected from solid particles having the property of absorbing biomolecules, such as, for example, affinity chromatography media, anion exchangers, hydrophobic interaction chromatography media, hydroxylapathite chromatography media, cation exchangers, metal affinity chromatography media, reversed-phase materials.

In another preferred embodiment, the chromatography media of the compounds not binding the biological sample (group NB) are selected from organic and/or inorganic acids, bases, salts, derivatives thereof or solvents of all types, and aqueous solutions thereof.

In another preferred embodiment, the agents for stabilisation of the biological sample are selected from, for example: glycerol, sucrose, sodium molybdate, ethylene glycols, urea, guanidinium chloride, betaine, taurine, DTE, DTT, EDTA, EGTA, monothioglycerol, detergents, polyethylene glycol (PEG), chloroform, methanol, H_2O, protease inhibitors.

In another preferred embodiment, the duration of the bringing into contact of the biological sample with the chromatography media can be freely selected.

In another preferred embodiment, the method is automated.

Embodiments of the invention also include kits for discovering suitable chromatography conditions in the separation of biological molecules by the above-described method which contain at least:

a) a multiwell plate which is defined by columns (X direction) and rows (Y direction) as matrix, where different chromatography media are arranged in a location-dependent manner on the matrix points of the plate defined by the matrix, and

b) different chromatography media for stocking the matrix points.

In another preferred embodiment, the kit contains software for the evaluation, identification and interpretation according to the above-described methods.